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SEQUENCE LISTING

<110> Imperial College Innovations Limited

<120> Therapeutically Useful Molecules

<130> 28646/42100

<140> PCT/GB2004/005100

<141> 2004-12-06

<150> GB 0328363.7

<151> 2003-12-06

<160> 18

<170> SeqWin99

<210> 1

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide of WT1 which is presented by HLA-A2 class I molecules

<400> 1

Arg Met Phe Pro Asn Ala Pro Tyr Leu

1 5

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1 of human TCR V -1.5 (V -8.2)

<400> 2

Ser Ser Tyr Ser Pro Ser

1 5

<210> 3

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2 of human TCR V -1.5 (V -8.2)

<400> 3

Tyr Thr Ser Ala Ala Thr Leu

1 5

<210> 4

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3 of human TCR V -1.5 (V -8.2) - 1

<400> 4  
Val Val Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr  
1 5 10

<210> 5  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CDR3 of human TCR V -1.5 (V -8.2) - 2

<400> 5  
Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr  
1 5 10

<210> 6  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CDR1 of human TCR V -2.1 (V -20.1)

<400> 6  
Asp Phe Gln Ala Thr Thr  
1 5

<210> 7  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CDR2 of human TCR V -2.1 (V -20.1)

<400> 7  
Ser Asn Glu Gly Ser Lys Ala  
1 5

<210> 8  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CDR3 of human TCR V -2.1 (V -20.1) - 1

<400> 8  
Ser Ala Arg Asp Gly Gly Glu Gly  
1 5

<210> 9  
<211> 11  
<212> PRT  
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<220>  
<223> CDR3 of human TCR V -2.1 (V -20.1) - 2

<400> 9  
Arg Asp Gly Gly Glu Gly Ser Glu Thr Gln Tyr  
1 5 10

<210> 10  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Framework amino acid sequence of constant portion C-terminal to CDR3  
  
 <400> 10  
 Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro  
 1 5 10  
  
 <210> 11  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Beginning of constant region of human TCR V -1.5 (V -8.2)  
  
 <400> 11  
 Tyr Ile Gln Asn Pro  
 1 5  
  
 <210> 12  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Beginning of framework amino acid sequence of human TCR V -2.1 (V -20.1)  
  
 <400> 12  
 Ser Glu Thr Gln Tyr  
 1 5  
  
 <210> 13  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Part of framework amino acid sequence of human TCR V -2.1 (V -20.1)  
  
 <400> 13  
 Phe Gly Pro Gly Thr Arg Leu Leu Val Leu  
 1 5 10  
  
 <210> 14  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Part of constant region of human TCR V -2.1 (V -20.1)  
  
 <400> 14  
 Glu Asp Leu Lys Asn  
 1 5  
  
 <210> 15

<211> 830  
 <212> DNA  
 <213> Human TCR V -1.5 (V -8.2)

<400> 15  
 atgctcctgc tgctcgtccc agtgctcgag gtgattttta ctctgggagg aaccagagcc 60  
 cagtcggtga cccagcttga cagccacgtc tctgtctctg aaggaacccc ggtgctgctg 120  
 aggtgcaact actcatcttc ttattcacca tctctcttct ggtatgtgca acaccccaac 180  
 aaaggactcc agcttctcct gaagtacaca tcagcggcca ccttgggttaa aggcataaac 240  
 ggttttgagg ctgaatttaa gaagagtga acctccttcc acctgacgaa accctcagcc 300  
 catatgagcg acgcggctga gtacttctgt gttgtgagtc ctttttcagg aggaggtgct 360  
 gacggactca cctttggcaa agggactcat ctaatcatcc agccctatat ccagaaccct 420  
 gaccctgccc tgtaccagct gagagactct aaatccagtg acaagtctgt ctgcctattc 480  
 accgattttg attctcaaac aaatgtgtca caaagtaagg attctgatgt gtatatcaca 540  
 gacaaaaactg tgctagacat gaggtctatg gacttcaaga gcaacagtg tggtggcctgg 600  
 agcaacaaat ctgactttgc atgtgcaaac gccttcaaca acagcattat tccagaagac 660  
 accttcttcc ccagcccaga aagtctcctgt gatgtcaagc tggtcgagaa aagctttgaa 720  
 acagatacga acctaaactt tcaaaacctg tcagtgattg gggtccgaat cctcctcctg 780  
 aaagtggccc ggtttaatct gctcatgacg ctgcggctgt ggtccagctg 830

<210> 16  
 <211> 276  
 <212> PRT  
 <213> Human TCR V -1.5 (V -8.2)

<400> 16  
 Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly  
 1 5 10 15  
 Gly Thr Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val  
 20 25 30  
 Ser Glu Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr  
 35 40 45  
 Ser Pro Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln  
 50 55 60  
 Leu Leu Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn  
 65 70 75 80  
 Gly Phe Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr  
 85 90 95  
 Lys Pro Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val  
 100 105 110  
 Ser Pro Phe Ser Gly Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly  
 115 120 125  
 Thr His Leu Ile Ile Gln Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val  
 130 135 140  
 Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe  
 145 150 155 160  
 Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp  
 165 170 175  
 Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe  
 180 185 190  
 Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys

195	200	205
Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro		
210	215	220
Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu		
225	230	235
Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg		
	245	250
		255
Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg		
	260	265
		270
Leu Trp Ser Ser		
275		

<210> 17  
 <211> 933  
 <212> DNA  
 <213> Human TCR V -2.1 (V -20.1)

<400> 17  
 atgctgctgc ttctgctgct tctggggcca ggctccgggc ttgggtgctgt cgtctctcaa 60  
 catccgagct ggggtatctg taagagtggg acctctgtga agatcgagtg ccgttccttg 120  
 gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg 180  
 atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgctga gaaggacaag 240  
 tttctcatca accatgcaag cctgacctg tccactctga cagtgaccag tgcccattct 300  
 gaagacagca gcttctacat ctgcagtgtc agagatgggg gggaggggtc ggagaccag 360  
 tacttcgggc caggcacgcg gctcctggtg ctcgaggacc tgaaaaacgt gttcccaccc 420  
 gaggtcgctg tgtttgagcc atcagaagca gagatctccc acacccaaaa ggccacactg 480  
 gtgtgcctgg ccacaggctt ctaccccgac cacgtggagc tgagctggtg ggtgaatggg 540  
 aaggaggtgc acagtgggtg cagcacagac ccgcagcccc tcaaggagca gcccgccttc 600  
 aatgactcca gatactgcct gagcagccgc ctgaggggtc cggccacctt ctggcagaac 660  
 ccccgcaacc acttccgctg tcaagtccag ttctacgggc tctcggagaa tgacgagtgg 720  
 acccaggata gggccaaaacc tgtcacccag atcgtcagcg ccgaggcctg gggtagagca 780  
 gactgtggct tcacctccga gtcttaccag caaggggtcc tgtctgccac catcctctat 840  
 gagatcttgc tagggaaggc caccctgtat gccgtgctgg tcagtgcctt cgtgctgatg 900  
 gccatggtca agagaaagga ttccagaggc tag 933

<210> 18  
 <211> 310  
 <212> PRT  
 <213> Human TCR V -2.1 (V -20.1)

<400> 18  
 Met Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala  
 1 5 10 15  
 Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser  
 20 25 30  
 Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe  
 35 40 45  
 Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser  
 50 55 60  
 Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys  
 65 70 75 80  
 Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr  
 85 90 95

Ser	Ala	His	Pro	Glu	Asp	Ser	Ser	Phe	Tyr	Ile	Cys	Ser	Ala	Arg	Asp		
			100					105					110				
Gly	Gly	Glu	Gly	Ser	Glu	Thr	Gln	Tyr	Phe	Gly	Pro	Gly	Thr	Arg	Leu		
		115					120					125					
Leu	Val	Leu	Glu	Asp	Leu	Lys	Asn	Val	Phe	Pro	Pro	Glu	Val	Ala	Val		
	130					135					140						
Phe	Glu	Pro	Ser	Glu	Ala	Glu	Ile	Ser	His	Thr	Gln	Lys	Ala	Thr	Leu		
145					150					155					160		
Val	Cys	Leu	Ala	Thr	Gly	Phe	Tyr	Pro	Asp	His	Val	Glu	Leu	Ser	Trp		
				165					170					175			
Trp	Val	Asn	Gly	Lys	Glu	Val	His	Ser	Gly	Val	Ser	Thr	Asp	Pro	Gln		
		180						185					190				
Pro	Leu	Lys	Glu	Gln	Pro	Ala	Leu	Asn	Asp	Ser	Arg	Tyr	Cys	Leu	Ser		
		195					200					205					
Ser	Arg	Leu	Arg	Val	Ser	Ala	Thr	Phe	Trp	Gln	Asn	Pro	Arg	Asn	His		
	210					215					220						
Phe	Arg	Cys	Gln	Val	Gln	Phe	Tyr	Gly	Leu	Ser	Glu	Asn	Asp	Glu	Trp		
225					230					235					240		
Thr	Gln	Asp	Arg	Ala	Lys	Pro	Val	Thr	Gln	Ile	Val	Ser	Ala	Glu	Ala		
				245					250					255			
Trp	Gly	Arg	Ala	Asp	Cys	Gly	Phe	Thr	Ser	Glu	Ser	Tyr	Gln	Gln	Gly		
		260						265					270				
Val	Leu	Ser	Ala	Thr	Ile	Leu	Tyr	Glu	Ile	Leu	Leu	Gly	Lys	Ala	Thr		
		275					280					285					
Leu	Tyr	Ala	Val	Leu	Val	Ser	Ala	Leu	Val	Leu	Met	Ala	Met	Val	Lys		
	290					295					300						
Arg	Lys	Asp	Ser	Arg	Gly												
305					310												